

The Impacts of a 4-lane Highway with Wildlife Underpasses on the Abundance and Genetic Structure of Black Bears in Eastern North Carolina



Jeremy Nicholson
M.S. Candidate

University of Tennessee
Department of Forestry, Wildlife,
and Fisheries



Introduction

- 4 million miles of roads in USA
- Never more than 22 miles from a road



Introduction

- Highways impact on wildlife:
 1. habitat fragmentation
 2. associated human development
 3. habitat loss
 4. direct mortality
 5. displacement and avoidance

Introduction

- Habitat fragmentation
 - disrupt movement patterns
 - alter social structure
 - small isolated populations

Introduction

- Mitigation efforts



Justification

- Few studies
- Effectiveness of mitigation efforts?



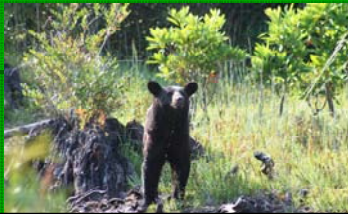
Justification



- Expansion of US Hwy 64
- Dissects prime wildlife habitat
- 3 wildlife underpasses

Justification

- Primary species of concern
- Black bears are ideal study species
- Umbrella species (Simberloff 1999)



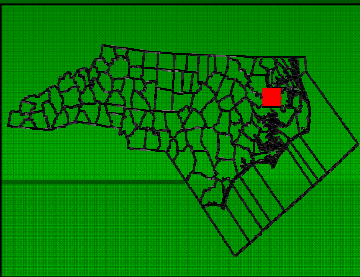
Justification

- 2000 – First phase began
- 2001 – Field work completed
- 2005 – Highway Construction completed
- May 2006 – 2nd phase began

Objectives

- Compare abundance and density of black bears between the 2 phases of the study
- Compare genetic structure of black bears between the 2 phases of the study
- Determine the mitigation value of the 3 wildlife underpasses

Study Area



Study Area



Study Area



Study Area



Methods

- Live trapping
 - Spring and Summer 06 & 07
 - Hair and tissue samples collected
 - Tooth samples
- Hair sampling
 - Fall 2006 (7 weeks)
- Hair sample analysis
 - Fall 07 and Spring 08

Livetrapping



Livetrapping

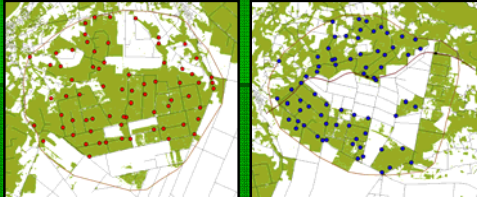


Livetrapping



Hair Sampling Design

- 70 hair-trap locations



Thompson 2003

Hair-Trap Design



Hair Collection

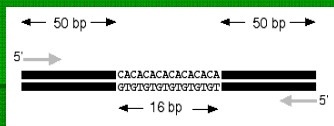


Selecting Samples

- 25 sample sites from each sampling period
- 1 sample from each site

Microsatellites

- 10 genetic markers
- Stretches of DNA that consist of tandem repeats of a simple sequence of nucleotides



- highly variable
- Uses Polymerase Chain Reaction (PCR)

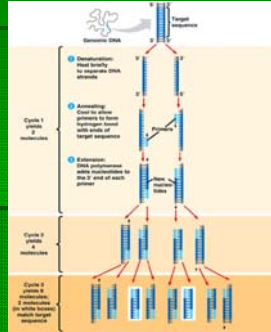
Hair Preparation and Analysis

- DNA extraction
- DNA Amplification
- PCR



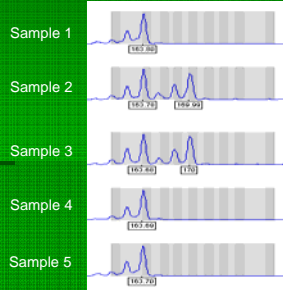
Polymerase Chain Reaction

- 20 million copies in 3 hours !



Genetic Analysis

- Fragment Analysis
 - Unique DNA profile



Population and Density Estimate

- Mark Recapture Experiments
- Advantages of noninvasive genetic sampling
 - increased capture probability
 - decreased tag loss
 - less intrusive

Probability of Identity

- "Shadow effect"

Table 4. Probability of identity estimates of black bears identified from hair samples on the treatment area, Washington County, North Carolina, 2000 (n = 53).

Locus	Number of alleles	Probability of identity	Probability of identity (collapsing)
G10C	4	0.096	0.700
G1A	5	0.124	0.417
G10B	6	0.123	0.419
G10M	6	0.088	0.391
G10K	4	0.279	0.547
G10L	9	0.040	0.335
G1D	5	0.175	0.470
M123	8	0.067	0.364
M120	8	0.089	0.290
G10P	5	0.114	0.413
Overall	6.0^a	1.07 x 10^{-6b}	2.73 x 10^{-6b}

^a Average number of alleles
^b Product of individual values

Thompson 2003

Mark-Recapture Studies

- Open population models
- Closed population models
 - multiple mark-recapture models

Population estimate

- Only closed models were considered
 - short time period (7 weeks)
 - No births occurred
 - deaths not likely significant
 - Immigration and emigration not significant

Multiple Mark-Recapture Models

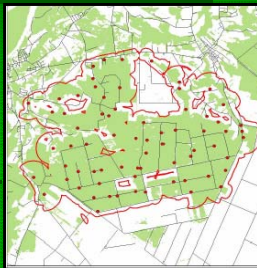
- Used with >2 sampling periods
- Equal Catchability Model (M_0 or null model) Assumes
 1. Population is closed
 2. Animals do not lose their marks
 3. All marks are recognized during each trapping session
 4. Every animal is at equal risk of capture

Multiple Mark-Recapture Models

- Models to relax the assumption of equal catchability
 - M_b
 - M_h
 - M_t
 - M_{tb} , M_{th} , M_{bh} , and M_{tbh}

Density Estimation

- $\text{Density} = (N) / \text{effective study size.}$



Thompson 2001

Genetic Structure

- Genetic Relatedness
- Heterozygosity
- Population Structure
 - Gene Flow
 - F_{ST}

Genetic Relatedness

- Proportion of shared alleles
 - Among individuals
 - Between study areas
 - Between subpopulations
 - Between north and south of the highway

Heterozygosity

- Measure of genetic variation
 - low levels

Population Structure

- Gene Flow - average number of migrants exchanged between local populations per generation (Nm)
- "One-migrant-per-generation" rule

Population Structure

- F_{ST}
 - Separate components of genetic variation into hierarchical levels:
 - Measures the reduction in heterozygosity of subpopulations relative to the total population

$$F_{ST} = (HT - HS) / HT$$

Comparing Results

	PRE CONSTRUCTION (Phase I, 2009-2011)	POST CONSTRUCTION (Phase II, 2015-2016)
TREATMENT AREA (Highway Construction)	DATA GROUP 1	DATA GROUP 2
CONTROL AREA (No Highway Construction)	DATA GROUP 3	DATA GROUP 4

Thompson 2003

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Questions ?